

RAW SEQUENCE LISTING

13

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/537,075
Source: PCT/10
Date Processed by STIC: 6/13/05

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,075

DATE: 06/13/2005

TIME: 09:38:34

Input Set : A:\12810-91 Sequence Listing.txt
 Output Set: N:\CRF4\06132005\J537075.raw

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3 <110> APPLICANT: Kesseler, Maria
4   Zelinski, Thomas
5   Hauer, Bernhard
7 <120> TITLE OF INVENTION: L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
9 <130> FILE REFERENCE: 12810-00091-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,075
C--> 11 <141> CURRENT FILING DATE: 2005-06-01
11 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/013367
12 <151> PRIOR FILING DATE: 2003-11-27
14 <150> PRIOR APPLICATION NUMBER: DE 102 56 381.0
15 <151> PRIOR FILING DATE: 2002-12-02
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2046
23 <212> TYPE: DNA
24 <213> ORGANISM: Escherichia coli
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27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (288)..(1121)
29 <223> OTHER INFORMATION: coding for rhaS (positive regulator of rhaBAD operon)
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33 <222> LOCATION: (1108)..(2043)
34 <223> OTHER INFORMATION: coding for rhaR (positive regulator of rhaRS operon)
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38 <222> LOCATION: (56)..(72)
39 <223> OTHER INFORMATION: potential RhaS binding site
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44 <223> OTHER INFORMATION: potential RhaS binding site
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47 <221> NAME/KEY: protein_bind
48 <222> LOCATION: (172)..(203)
49 <223> OTHER INFORMATION: potential RhaR binding site
51 <220> FEATURE:
52 <221> NAME/KEY: protein_bind
53 <222> LOCATION: (210)..(241)
54 <223> OTHER INFORMATION: potential RhaR binding site
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature

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59 <223> OTHER INFORMATION: potential start of transcription (complement)
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63 cacaatttgc tgaatttgtgg tcatgtatgtt ctcaccgcatttccctgaaaa ttcacgctgt 180
64 atcttgaaaa atcgacgttt ttacgtggt ttccgtcga aaatttaagg taagaacctg 240
65 acctcgttatg tactatttcg ccgtgttgc gacatcagga ggccagtatg accgtattac 300
66 atatgttggat ttttttccg tctggtaacg cgtccgtggc gatagaaccc cggctcccgc 360
67 aggccgattt tcctgaacat catcatgatt ttcatgaaat tgtgattgtc gaacatggca 420
68 cggttattca tgtgtttaat gggcagccct ataccatcac cgggtggcaacg gtctgtttcg 480
69 tacgcgatca tgatcgcat ctgtatgaac ataccgataa tctgtgtctg accaatgtgc 540
70 tgtatcgctc gccggatcgatca tttcagtttc tcgccccggct gaatcagttt ctgcacaag 600
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73 gtcgcgagat cttgtttatg caattactgc tcttgcgtcg taaaaggcgt ttgcaggaga 780
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78 gctgtggatt cagcgcacatca aaccactttt cgacgtttt tcgcccggag ttaactgg 1080
79 caccgcgtga tattcgccag ggacgggatg gctttctgca ataacgcgaa tcttctcaac 1140
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86 ggggcatttc cgggatttaa cggccagcgc gggcaaccac actggcgtt agtagcatg 1560
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91 gcatcgatca gtgagcgcgt ttgcgtca gatattgc acgagactgg aatgaccatc 1860
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93 ctgttaatca gtgatatttc gaccgaatgt ggcttgaag atagtaacta ttttcgggtg 1980
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97 <211> LENGTH: 287
98 <212> TYPE: DNA .
99 <213> ORGANISM: Escherichia coli
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104 <222> LOCATION: (1)..(287)
105 <223> OTHER INFORMATION: rhaBAD promoter fragment containing rhaS and rhaR binding sites
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108 taaattttcg acggaaaacc acgtaaaaaaaaa cgtcgatttt tcaagataca gctgtatcc 120

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RAW SEQUENCE LISTING DATE: 06/13/2005
 PATENT APPLICATION: US/10/537,075 TIME: 09:38:34

Input Set : A:\12810-91 Sequence Listing.txt
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109 tcaggaaatg cggtagcat cacatcacca caattcagca aattgtgaac atcatcacgt 180
 110 tcatcttcc ctgggtgcca atggcccatt ttcctgtcg taacgagaag gtcgcgaatt 240
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 115 <211> LENGTH: 125
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 117 <213> ORGANISM: Escherichia coli
W--> 118 <220> FEATURE:
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 120 <222> LOCATION: (1)..(125)
 121 <223> OTHER INFORMATION: rhaBAD promoter fragment containing RhaS binding site
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 129 <211> LENGTH: 123
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 143 <211> LENGTH: 51
 144 <212> TYPE: DNA
 145 <213> ORGANISM: Escherichia coli
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 148 <222> LOCATION: (1)..(51)
 149 <223> OTHER INFORMATION: palindromic RhaS binding site of rhaBAD promoter
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 155 <211> LENGTH: 1071
 156 <212> TYPE: DNA
 157 <213> ORGANISM: Alcaligenes faecalis
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 160 <222> LOCATION: (1)..(1068)
 161 <223> OTHER INFORMATION: coding for nitrilase
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 164 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser
 165 1 5 10 15

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166 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct	96
167 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala	
168 20 25 30	
169 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc	144
170 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr	
171 35 40 45	
172 tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg	192
173 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp	
174 50 55 60	
175 tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac	240
176 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp	
177 65 70 75 80	
178 agt gca gag ttt caa cgc att gcc cag gcc gca ccg acc ttg ggt att	288
179 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile	
180 85 90 95	
181 ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg	336
182 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu	
183 100 105 110	
184 ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384
185 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg	
186 115 120 125	
187 aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432
188 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr	
189 130 135 140	
190 gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct	480
191 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala	
192 145 150 155 160	
193 cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac	528
194 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr	
195 165 170 175	
196 tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta	576
197 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu	
198 180 185 190	
199 tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc	624
200 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala	
201 195 200 205	
202 tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc	672
203 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser	
204 210 215 220	
205 agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac	720
206 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His	
207 225 230 235 240	
208 aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg	768
209 Asn Ala Pro Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe Ala	
210 245 250 255	
211 ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc	816
212 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly	
213 260 265 270	
214 ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg	864

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Input Set : A:\12810-91 Sequence Listing.txt
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215	Leu	Ile	Ile	Ala	Asp	Leu	Asn	Met	Glu	Glu	Ile	Ala	Phe	Ala	Lys	Ala	
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218	Ile	Asn	Asp	Pro	Val	Gly	His	Tyr	Ser	Lys	Pro	Glu	Ala	Thr	Arg	Leu	
219	290				295					300							
220	gtg	ctg	gac	ttg	ggg	cac	cga	gac	ccc	atg	act	cg	gtg	cac	tcc	aaa	960
221	Val	Leu	Asp	Leu	Gly	His	Arg	Asp	Pro	Met	Thr	Arg	Val	His	Ser	Lys	
222	305				310				315				320				
223	agc	gtg	acc	agg	gaa	gag	gct	ccc	gag	caa	ggt	gtg	caa	agc	aag	att	1008
224	Ser	Val	Thr	Arg	Glu	Glu	Ala	Pro	Glu	Gln	Gly	Val	Gln	Ser	Lys	Ile	
225	325				330				330				335				
226	gcc	tca	gtc	gct	atc	agc	cat	cca	cag	gac	tcg	gac	aca	ctg	cta	gtg	1056
227	Ala	Ser	Val	Ala	Ile	Ser	His	Pro	Gln	Asp	Ser	Asp	Thr	Leu	Leu	Val	
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241	Pro	Asn	Tyr	Asp	Leu	Ala	Thr	Gly	Val	Asp	Lys	Thr	Ile	Glu	Leu	Ala	
242					20				25				30				
243	Arg	Gln	Ala	Arg	Asp	Glu	Gly	Cys	Asp	Leu	Ile	Val	Phe	Gly	Glu	Thr	
244					35				40				45				
245	Trp	Leu	Pro	Gly	Tyr	Pro	Phe	His	Val	Trp	Leu	Gly	Ala	Pro	Ala	Trp	
246					50				55				60				
247	Ser	Leu	Lys	Tyr	Ser	Ala	Arg	Tyr	Tyr	Ala	Asn	Ser	Leu	Ser	Leu	Asp	
248					65				70				75			80	
249	Ser	Ala	Glu	Phe	Gln	Arg	Ile	Ala	Gln	Ala	Ala	Arg	Thr	Leu	Gly	Ile	
250					85				90				95				
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252					100				105				110				
253	Gly	Gln	Cys	Leu	Ile	Asp	Asp	Lys	Gly	Glu	Met	Leu	Trp	Ser	Arg	Arg	
254					115				120				125				
255	Lys	Leu	Lys	Pro	Thr	His	Val	Glu	Arg	Thr	Val	Phe	Gly	Glu	Gly	Tyr	
256					130				135				140				
257	Ala	Arg	Asp	Leu	Ile	Val	Ser	Asp	Thr	Glu	Leu	Gly	Arg	Val	Gly	Ala	
258					145				150				155			160	
259	Leu	Cys	Cys	Trp	Glu	His	Leu	Ser	Pro	Leu	Ser	Lys	Tyr	Ala	Leu	Tyr	
260					165				170				175				
261	Ser	Gln	His	Glu	Ala	Ile	His	Ile	Ala	Ala	Trp	Pro	Ser	Phe	Ser	Leu	
262					180				185				190				
263	Tyr	Ser	Glu	Gln	Ala	His	Ala	Leu	Ser	Ala	Lys	Val	Asn	Met	Ala	Ala	
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265	Ser	Gln	Ile	Tyr	Ser	Val	Glu	Gly	Gln	Cys	Phe	Thr	Ile	Ala	Ala	Ser	

VERIFICATION SUMMARY
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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